

SEQUENCE LISTING

<110> Shionogi & Co., LTD.

<120> A gene encoding novel human secretory type  
phospholipase A2

<130> 51-06052W0

<150> JP 266616/1999

<151> 1999-09-21

<160> 34

<170> PatentIn Ver. 2.0

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gctatggccg cctggagaan ctggctgtg accccaagct ggaaaagtac ctttctcta 180

tcactcgaga caacatcttc tgtgctgta aaacggcttg ccageggcat acctgcgaat 240

gtgacaaaaa accgctctct gcttcgcca caacctgaac acttacaacc gcaantatgc 300

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<222> (166)..(591)

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actcggtccc catcaccttt gcaacaggga cagagcttgc agtaccaggaa tgccctggg 120

agttggcaga gcaggctccc atgccccctg cctacccccc ccagg atg aaa cct ccc 177

Met Lys Pro Pro

att gcc ctg gct tgc ctt tgc ctc ctg gtg ccc ctg gct ggc ggg aac 225

Ile Ala Leu Ala Cys Leu Cys Leu Val Pro Leu Ala Gly Gly Asn

-15 -10 -5 -1 1

ctg gtc cag ttt gga gtg atg att gag aga atg acg gga aag cct gcc 273

Leu Val Gln Phe Gly Val Met Ile Glu Arg Met Thr Gly Lys Pro Ala

5 10 15

ctg cag tac aat gac tat ggc tgc tat tgc ggt gtc ggt ggc tcc cac 321

Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Val Gly Ser His

20 25 30

tgg cca gtg gac gag acg gat tgg tgt tgt cat gcc cat gac tgc tgc 369

Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala His Asp Cys Cys

35 40 45

tat ggc cgc ctg gag aag ctg ggc tgt gac ccc aag ctg gaa aag tac 417

Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys Leu Glu Lys Tyr

50 55 60 65

ctc ttc tct atc act cga gac aac atc ttc tgt gct ggt aga acg gct 465

Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala Gly Arg Thr Ala

70 75 80

tgc cag cgg cat acc tgc gag tgt gac aag aga gct gct ctt tgc ttt 513

Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala Ala Leu Cys Phe

85 90 95

cgc cac aac ctg aac act tac aac cgc aag tat gcc cac tac ccc aac 561

Arg His Asn Leu Asn Thr Tyr Asn Arg Lys Tyr Ala His Tyr Pro Asn

100

105

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aag ctg tgt act ggg ccc acc cca ccc tgc tgaggccctg ctggctcca 611  
Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys

115

120

tagccacccc aggctgctgc agtctcaggc ccagagaagc tcggaaaccca gattctctc 671

ccagcagact catccccccc cccccccaga gatcatgagc octggctctt ggctccagg 731

accacaccag atccacggga tcagctgaag aagtacggg actcgctagc gtcacaaga 791

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cgaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 883

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<213> Mus musculus

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Gly Lys Pro Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Val  
15 20 25

Gly Gly Ser His Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala  
30 35 40 45

His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys  
50 55 60

Leu Glu Lys Tyr Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala  
65 70 75

Gly Arg Thr Ala Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala  
80 85 90

Ala Leu Cys Phe Arg His Asn Leu Asn Thr Tyr Asn Arg Lys Tyr Ala  
95 100 105

His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys  
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tcctggaga aggagggaaag cctggggca cctggaaaat tcaggctgtat ctctccctcg 180  
ggctactttg ggctcgnggg ccccgagcag ccctgggtcc agcccagcgt ggctcacagg 240  
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<400> 22

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<400> 23

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Met Lys Ser Pro His Val Leu Val Phe Leu Cys Leu Leu Val Ala Leu

-15

-10

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gtc acc ggg aac ctg gtt cag ttt ggg gtg atg atc gag aag atg aca 154  
Val Thr Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Lys Met Thr  
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ggc aag tcc gcc ctg cag tac aac gac tat ggc tgt tac tgc ggc atc 202  
Gly Lys Ser Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Ile  
15 20 25

ggt ggc tcc cac tgg ccg gtg gac cag act gac tgg tgc tgc cac gcc 250  
Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala  
30 35 40 45

cac gac tgc tgc tac ggg cgt ctg gag aag ctg ggc tgt gag ccc aaa 298  
His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys  
50 55 60

ctg gaa aag tat ctt ttc tct gtc agc gaa cgt ggc att ttc tgc gcc 346  
Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala  
65 70 75

ggc agg acc acc tgc cag cgg ctg acc tgc gag tgt gac aag agg gct 394  
Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala  
80 85 90

gcc ctc tgc ttt cgc cgc aac ctg ggc acc tac aac cgc aaa tat gcc 442  
Ala Leu Cys Phe Arg Arg Asn Leu Gly Thr Tyr Asn Arg Lys Tyr Ala  
95 100 105

cat tat ccc aac aag ctg tgc acc ggg ccc acc cog ccc tgc tga 487  
His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys  
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Val Thr Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Lys Met Thr  
-1 1 5 10

Gly Lys Ser Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Ile  
15 20 25

Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala

30                    35                    40                    45

His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys  
                   50                  55                  60

Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala  
65 70 75

Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala  
80 85 90

Ala Leu Cys Phe Arg Arg Asn Leu Gly Thr Tyr Asn Arg Lys Tyr Ala  
95 100 105

His Tyr Pro Asn Lys Leu Cys Thr Gly Pro Thr Pro Pro Cys  
110 115 120

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<400> 34

taagctttc tagatcagca gggggggtg ggcccggtgc acag

44